

# SEQUENCE LISTING

<110> Johnson, Leslie S.  
Li, Hua  
Tuailon, Nadine

<120> SOLUBLE FC R FUSION PROTEINS AND METHODS OF USE THEREOF

<130> 11183-005-999

<140> TBA

<141>

<150> 60/439,709

<151> 2003-01-13

<160> 42

<170> PatentIn version 3.0

<210> 1

<211> 420

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIa-G2

<400> 1

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Trp	Tyr	Arg	Val	Leu	Glu	Lys	Asp	Ser	Val	Thr	Leu	Lys	Cys	Gln	Gly	20	25	30	
Ala	Tyr	Ser	Pro	Glu	Asp	Asn	Ser	Thr	Gln	Trp	Phe	His	Asn	Glu	Ser	35	40	45	
Leu	Ile	Ser	Ser	Gln	Ala	Ser	Ser	Tyr	Phe	Ile	Asp	Ala	Ala	Thr	Val	50	55	60	
Asp	Asp	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Thr	Asn	Leu	Ser	Thr	Leu	Ser	65	70	75	80
Asp	Pro	Val	Gln	Leu	Glu	Val	His	Ile	Gly	Trp	Leu	Leu	Leu	Gln	Ala	85	90	95	
Pro	Arg	Trp	Val	Phe	Lys	Glu	Glu	Asp	Pro	Ile	His	Leu	Arg	Cys	His	100	105	110	

Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly  
 115 120 125  
 Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys  
 130 135 140  
 Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly  
 145 150 155 160  
 Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln Gly  
 165 170 175  
 Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln Val  
 180 185 190  
 Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val  
 195 200 205  
 Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 210 215 220  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 225 230 235 240  
 His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu  
 245 250 255  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr  
 260 265 270  
 Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn  
 275 280 285  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro  
 290 295 300  
 Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln  
 305 310 315 320  
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 325 330 335  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 340 345 350  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 355 360 365  
 Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 370 375 380  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 385 390 395 400  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 405 410 415  
 Ser Pro Gly Lys  
 420

<210> 2

<211> 409

<212> PRT

<213> homo sapiens

<220>

<223> sFcRIIb-G2

<400> 2

Thr	Pro	Ala	Ala	Pro	Pro	Lys	Ala	Val	Leu	Lys	Leu	Glu	Pro	Gln	Trp	
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Ile	Asn	Val	Leu	Gln	Glu	Asp	Ser	Val	Thr	Leu	Thr	Cys	Arg	Gly	Thr	
			20					25					30			
His	Ser	Pro	Glu	Ser	Asp	Ser	Ile	Gln	Trp	Phe	His	Asn	Gly	Asn	Leu	
		35					40					45				
Ile	Pro	Thr	His	Thr	Gln	Pro	Ser	Tyr	Arg	Phe	Lys	Ala	Asn	Asn	Asn	
	50					55					60					
Asp	Ser	Gly	Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp	
65					70					75					80	
Pro	Val	His	Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro	
			85						90					95		
His	Leu	Glu	Phe	Gln	Glu	Gly	Glu	Thr	Ile	Val	Leu	Arg	Cys	His	Ser	
			100					105					110			
Trp	Lys	Asp	Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys	
		115					120						125			
Ser	Lys	Lys	Phe	Ser	Arg	Ser	Asp	Pro	Asn	Phe	Ser	Ile	Pro	Gln	Ala	
	130					135					140					
Asn	His	Ser	His	Ser	Gly	Asp	Tyr	His	Cys	Thr	Gly	Asn	Ile	Gly	Tyr	
145					150					155					160	
Thr	Leu	Phe	Ser	Ser	Lys	Pro	Val	Thr	Ile	Thr	Val	Gln	Ala	Pro	Ser	
				165				170						175		
Ser	Ser	Pro	Met	Glu	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	
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Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
		195					200					205				
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
	210					215					220					
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	
225					230					235					240	
Val	Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
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Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His  
                   260                                  265                                  270  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
                   275                                  280                                  285  
 Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln  
                   290                                  295                                  300  
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met  
   305                                  310                                  315                                  320  
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
                                   325                                  330                                  335  
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
                   340                                  345                                  350  
 Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu  
                   355                                  360                                  365  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
                   370                                  375                                  380  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
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 Lys Ser Leu Ser Leu Ser Pro Gly Lys  
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<210> 3

<211> 409

<212> PRT

<213> Homo sapiens

<220> :

<223> sFcRIIa(131R)-G2

<400> 3

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 Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro  
                   20                                  25                                  30  
 Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr  
                   35                                  40                                  45  
 His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly  
   50                                  55                                  60  
 Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His  
   65                                  70                                  75                                  80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu  
                             85                            90                            95  
 Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp  
                             100                            105                            110  
 Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys  
                             115                            120                            125  
 Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser  
                             130                            135                            140  
 His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe  
                             145                            150                            155                            160  
 Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser  
                             165                            170                            175  
 Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys  
                             180                            185                            190  
 Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
                             195                            200                            205  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
                             210                            215                            220  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr  
                             225                            230                            235                            240  
 Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
                             245                            250                            255  
 Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His  
                             260                            265                            270  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
                             275                            280                            285  
 Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln  
                             290                            295                            300  
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met  
                             305                            310                            315                            320  
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
                             325                            330                            335  
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
                             340                            345                            350  
 Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu  
                             355                            360                            365  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
                             370                            375                            380  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
                             385                            390                            395                            400  
 Lys Ser Leu Ser Leu Ser Pro Gly Lys

405

<210> 4

<211> 409

<212> PRT

<213> homo sapiens

<220>

<223> sFcRIIa(131H) -G2

<400> 4

Ala	Pro	Pro	Lys	Ala	Val	Leu	Lys	Leu	Glu	Pro	Pro	Trp	Ile	Asn	Val	1	5	10	15
Leu	Gln	Glu	Asp	Ser	Val	Thr	Leu	Thr	Cys	Gln	Gly	Ala	Arg	Ser	Pro	20	25	30	
Glu	Ser	Asp	Ser	Ile	Gln	Trp	Phe	His	Asn	Gly	Asn	Leu	Ile	Pro	Thr	35	40	45	
His	Thr	Gln	Pro	Ser	Tyr	Arg	Phe	Lys	Ala	Asn	Asn	Asn	Asp	Ser	Gly	50	55	60	
Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp	Pro	Val	His	65	70	75	80
Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro	His	Leu	Glu	85	90	95	
Phe	Gln	Glu	Gly	Glu	Thr	Ile	Met	Leu	Arg	Cys	His	Ser	Trp	Lys	Asp	100	105	110	
Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys	Ser	Gln	Lys	115	120	125	
Phe	Ser	His	Leu	Asp	Pro	Thr	Phe	Ser	Ile	Pro	Gln	Ala	Asn	His	Ser	130	135	140	
His	Ser	Gly	Asp	Tyr	His	Cys	Thr	Gly	Asn	Ile	Gly	Tyr	Thr	Leu	Phe	145	150	155	160
Ser	Ser	Lys	Pro	Val	Thr	Ile	Thr	Val	Gln	Val	Pro	Ser	Met	Gly	Ser	165	170	175	
Ser	Ser	Pro	Met	Glu	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	180	185	190	
Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	195	200	205	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	210	215	220	
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	225	230	235	240

Val	Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu			
				245					250					255				
Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His			
			260					265					270					
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys			
		275					280					285						
Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln			
	290					295					300							
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met			
305					310					315					320			
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro			
			325					330						335				
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn			
			340					345					350					
Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu			
		355					360					365						
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val			
	370					375					380							
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln			
385					390					395					400			
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys										
				405														

<210> 5

<211> 1382

<212> DNA

<213> homo sapiens

<220>

<223> sFcRIIB insert with signal sequence

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ggctcctggt gctgggacac ctgcagctcc cccaaaggct gtgctgaaac tcgagcccca	180
gtggatcaac gtgctccagg aggactctgt gactctgaca tgccggggga ctcacagccc	240
tgagagcgac tccattcagt ggttccacaa tgggaatctc attcccaccc acacgcagcc	300
cagctacagg ttcaaggcca acaacaatga cagcggggag tacacgtgcc agactggcca	360

gaccagcctc agcgaccctg tgcattctgac tgtgctttct gagtggtctg tgctccagac	420
ccctcacctg gagttccagg agggagaaac catcgtgctg aggtgccaca gctggaagga	480
caagcctctg gtcaagggtca cattcttcca gaatggaaaa tccaagaaat tttcccgttc	540
ggatcccaac ttctccatcc cacaagcaaa ccacagtcac agtggtgatt accactgcac	600
aggaaacata ggctacacgc tgttctcatc caagcctgtg accatcactg tccaagctcc	660
cagctcttca cccatggagg agcgcaaagt ttgtgtcgag tgcccaccgt gccagcacc	720
acctgtggca ggaccgtcag tcttcctttt cccccaaaa cccaaggaca ccctcatgat	780
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ccagttcaac tgggtacgtg acggcatgga ggtgcataat gccaaagaca agccacggga	900
ggagcagttc aacagcacgt tccgtgtgtt cagcgtcttc accgtcgtgc accaggactg	960
gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa ggctcccag ccccatcga	1020
gaaaaccatc tccaaaacca aagggcagcc ccgagaacca caggtgtaca ccctgcccc	1080
atcccgggag gagatgacca agaaccaggt cagcctgacc tgcttgggtca aaggcttcta	1140
ccccagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac	1200
cacacctccc atgctggact ccgacggctc cttcttcttc tacagcaagc tcaccgtgga	1260
caagagcagg tggcagcagg ggaacgtctt ctcatgctct gtgatgcatg aggctctgca	1320
caaccactac acacagaaga gcctctccct gtctccgggt aaatgagtgc ggccgcgaat	1380
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<211> 1418

<212> DNA

<213> homo sapiens

<220>

<223> sFcRIIIA insert

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ctccacaggt gtccactcca tgcggactga agatctcccc aaggctgtgg tgttcctgga	180
gcctcaatgg tacaggggtg tcgagaagga cagtgtgact ctgaagtgcc agggagccta	240
ctcccctgag gacaattcca cacagtgggt tcacaatgag agcctcatct caagccaggc	300



ctcgagctac	ttcattgacg	ctgccacagt	cgacgacagt	ggagagtaca	ggtgccagac	360
aaacctctcc	accctcagtg	acccggtgca	gctagaagtc	catatcggct	ggctgttgct	420
ccaggccccct	cggtgggtgt	tcaaggagga	agaccctatt	cacctgaggt	gtcacagctg	480
gaagaacact	gctctgcata	aggtcacata	tttacagaat	ggcaaaggca	ggaagtatct	540
tcatcataat	tctgacttct	acattccaaa	agccacactc	aaagacagcg	gctcctactt	600
ctgcaggggg	cttgttgga	gtaaaaatgt	gtcttcagag	actgtgaaca	tcaccatcac	660
tcaaggtttg	gcagtgtcaa	ccatctcatc	attctttcca	cctgggtacc	aagtcgagcg	720
caaatgttgt	gtcgagtgcc	caccgtgccc	agcaccacct	gtggcaggac	cgtcagtctt	780
cctcttcccc	ccaaaaccca	aggacacct	catgatctcc	cggaccctg	aggtcacgtg	840
cgtggtggtg	gacgtgagcc	acgaagaccc	cgagggtccag	ttcaactgg	acgtggacgg	900
catggaggtg	cataatgcca	agacaaagcc	acgggaggag	cagttcaaca	gcacgttccg	960
tgtggtcagc	gtcctcaccg	tcgtgcacca	ggactggctg	aacggcaagg	agtacaagtg	1020
caaggtctcc	aacaaaggcc	tcccagcccc	catcgagaaa	accatctcca	aaaccaagg	1080
gcagccccga	gaaccacagg	tgtacacct	gccccatcc	cgggaggaga	tgaccaagaa	1140
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ggagagcaat	gggcagccgg	agaacaacta	caagaccaca	cctcccatgc	tggactccga	1260
cggctccttc	ttcctctaca	gcaagctcac	cgtggacaag	agcagggtggc	agcaggggaa	1320
cgtcttctca	tgtccgtga	tgcattgaggc	tctgcacaac	cactacacac	agaagagcct	1380
ctccctgtct	ccgggtaaat	gagtgcggcc	gcgaattc			1418

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<211> 1391

<212> DNA

<213> homo sapiens

<220>

<223> sFcRIIA-131H

<400> 7

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ggctcctgtt	gctgggacac	ctgcagctcc	cccaaaggct	gtgctgaaac	ttgagcccc	180
gtggatcaac	gtgctccagg	aggactctgt	gactctgaca	tgccaggggg	ctcgcagccc	240

tgagagcgac	tccattcagt	ggttccacaa	tgggaatctc	attcccaccc	acacgcagcc	300
cagctacagg	ttcaaggcca	acaacaatga	cagcggggag	tacacgtgcc	agactggcca	360
gaccagcctc	agcgaccctg	tgcattctgac	tgtgcttttc	gaatggctgg	tgctccagac	420
ccctcacctg	gagttccagg	agggagaaa	catcatgctg	aggtgccaca	gctggaagga	480
caagcctctg	gtcaagggtca	cattcttcca	gaatggaaaa	tcccagaaat	tctcccattt	540
ggatcccacc	ttctccatcc	cacaagcaaa	ccacagtcac	agtgggtgatt	accactgcac	600
aggaaacata	ggctacacgc	tgttctcatc	caagcctgtg	accatcactg	tccaagtgcc	660
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cccagcacca	cctgtggcag	gaccgtcagt	cttcctcttc	ccccaaaaac	ccaaggacac	780
cctcatgata	tcccggaccc	ctgaggtcac	gtgctgggtg	gtggacgtga	gccacgaaga	840
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gccacgggag	gagcagttca	acagcacgtt	ccgtgtggtc	agcgtcctca	ccgtcgtgca	960
ccaggactgg	ctgaacggca	aggagtacaa	gtgcaaggtc	tccaacaaag	gcctcccagc	1020
ccccatcgag	aaaaccatct	ccaaaaccaa	agggcagccc	cgagaaccac	aggtgtacac	1080
cctgccccca	tcccgggagg	agatgaccaa	gaaccaggtc	agcctgacct	gcctgggtcaa	1140
aggcttctac	cccagcgaca	tgcctgtgga	gtgggagagc	aatgggcagc	cggagaacaa	1200
ctacaagacc	acacctccca	tgctggactc	cgacggctcc	ttcttctctt	acagcaagct	1260
caccgtggac	aagagcaggt	ggcagcaggg	gaacgtcttc	tcatgctctg	tgatgcatga	1320
ggctctgcac	aaccactaca	cacagaagag	cctctccctg	tctccgggta	aatgagtgcg	1380
gccgcgaatt	c					1391

<210> 8

<211> 1391

<212> DNA

<213> homo sapiens

<220>

<223> sFcRIIA-131R

<400> 8

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tgactgcaag	tccccccagc	cttgggggtca	tatgcttctg	tggacagctg	tgctattcct	120
ggctcctgtt	gctgggacac	ctgcagctcc	cccaaaggct	gtgctgaaac	ttgagccccc	180

gtggatcaac	gtgctccagg	aggactctgt	gactctgaca	tgccaggggg	ctcgagccc	240
tgagagcgac	tccattcagt	ggttcacaa	tgggaatctc	attcccaccc	acacgcagcc	300
cagctacagg	ttcaaggcca	acaacaatga	cagcggggag	tacacgtgcc	agactggcca	360
gaccagcctc	agcgaccctg	tgcactctgac	tgtgcttttc	gaatggctgg	tgctccagac	420
ccctcacctg	gagttccagg	agggagaaac	catcatgctg	aggtgccaca	gctggaagga	480
caagcctctg	gtcaagggtca	cattcttcca	gaatggaaaa	tcccagaaat	tctcccgttt	540
ggatcccacc	ttctccatcc	cacaagcaaa	ccacagtcac	agtgggtgatt	accactgcac	600
aggaaacata	ggctacacgc	tgttctcatc	caagcctgtg	accatcactg	tccaagtgcc	660
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<220>

<223> human FCRIIa

<400> 9

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 Ser Gln Ala Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro  
 35 40 45  
 Trp Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly  
 50 55 60  
 Ala Arg Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn  
 65 70 75 80  
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 85 90 95  
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 100 105 110  
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 Pro His Leu Glu Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His  
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 Ser Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly  
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 Lys Ser Gln Lys Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln  
 165 170 175  
 Ala Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly  
 180 185 190  
 Tyr Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro  
 195 200 205  
 Ser Met Gly Ser Ser Ser Pro Met Gly Ile Ile Val Ala Val Val Ile  
 210 215 220  
 Ala Thr Ala Val Ala Ala Ile Val Ala Ala Val Val Ala Leu Ile Tyr  
 225 230 235 240  
 Cys Arg Lys Lys Arg Ile Ser Ala Asn Ser Thr Asp Pro Val Lys Ala  
 245 250 255  
 Ala Gln Phe Glu Pro Pro Gly Arg Gln Met Ile Ala Ile Arg Lys Arg  
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 Gln Leu Glu Glu Thr Asn Asn Asp Tyr Glu Thr Ala Asp Gly Gly Tyr  
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 <211> 83  
 <212> PRT  
 <213> homo sapiens  
 <220>  
 <223> Membrane proximal domain of RIIIa

<400> 20

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Glu Glu Asp Pro Ile His Leu Arg Cys His Ser Trp Lys Asn Thr Ala  
20 25 30  
Leu His Lys Val Thr Tyr Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe  
35 40 45  
His His Asn Ser Asp Phe Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser  
50 55 60  
Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly Ser Lys Asn Val Ser Ser  
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Glu Thr Val

<210> 21

<211> 78

<212> PRT

<213> homo sapiens

<220>

<223> Membrane proximal domain of RIIB

<400> 21

Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln  
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Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp Lys Pro  
20 25 30  
Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys Phe Ser  
35 40 45  
Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser His Ser  
50 55 60  
Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe  
65 70 75

<210> 22

<211> 78

<212> PRT

<213> homo sapiens

<220>



<223> Membrane proximal domain of RIIa(131R)

<400> 22

Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln  
1 5 10 15

Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp Lys Pro  
20 25 30

Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys Phe Ser  
35 40 45

Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser His Ser  
50 55 60

Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe  
65 70 75

<210> 23

<211> 78

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<223> Membrane proximal domain of RIIa(131H)

<400> 23

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1 5 10 15

Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp Lys Pro  
20 25 30

Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys Phe Ser  
35 40 45

His Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser His Ser  
50 55 60

Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe  
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<212> DNA

<213> homo sapiens

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<223> human FcRIIIa

<400> 24

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ctggagcctc aatggtacag ggtgctcgag aaggacagtg tgactctgaa gtgccaggga      180
gcctactccc ctgaggacaa ttccacacag tggtttcaca atgagagcct catctcaagc      240
caggcctcga gctacttcat tgacgtgcc acagtcgacg acagtggaga gtacaggtgc      300
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gacctcaag acaaatgacc cccatcccat gggggtaata agagcagtag cagcagcatc      840
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<210> 25

<211> 254

<212> PRT

<213> homo sapiens

<220>

<223> human FcRIIIa

<400> 25

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Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
          20           25           30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
          35           40           45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
          50           55           60
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Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr  
 65 70 75 80  
 Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu  
 85 90 95  
 Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln  
 100 105 110  
 Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys  
 115 120 125  
 His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn  
 130 135 140  
 Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro  
 145 150 155 160  
 Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe  
 165 170 175  
 Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln  
 180 185 190  
 Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln  
 195 200 205  
 Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly  
 210 215 220  
 Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp  
 225 230 235 240  
 Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys  
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<211> 1393

<212> DNA

<213> homo sapiens

<220>

<223> human FcRIIB2

<400> 26

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 atgcttctgt ggacagctgt gctattcctg gctcctgttg ctgggacacc tgcagctccc 180  
 ccaaaggctg tgctgaaact cgagccccag tggatcaacg tgctccagga ggactctgtg 240  
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<211> 291

<212> PRT

<213> homo sapiens

<220>

<223> human FCRIIB

<400> 27

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Ala Asp Cys Lys Ser Pro Gln Pro Trp Gly His Met Leu Leu Trp Thr
          20           25           30

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Ala Val Leu Phe Leu Ala Pro Val Ala Gly Thr Pro Ala Ala Pro Pro  
 35 40 45  
 Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val Leu Gln Glu  
 50 55 60  
 Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro Glu Ser Asp  
 65 70 75 80  
 Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr His Thr Gln  
 85 90 95  
 Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly Glu Tyr Thr  
 100 105 110  
 Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His Leu Thr Val  
 115 120 125  
 Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln Glu  
 130 135 140  
 Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp Lys Pro Leu  
 145 150 155 160  
 Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys Phe Ser Arg  
 165 170 175  
 Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser His Ser Gly  
 180 185 190  
 Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe Ser Ser Lys  
 195 200 205  
 Pro Val Thr Ile Thr Val Gln Ala Pro Ser Ser Ser Pro Met Gly Ile  
 210 215 220  
 Ile Val Ala Val Val Thr Gly Ile Ala Val Ala Ala Ile Val Ala Ala  
 225 230 235 240  
 Val Val Ala Leu Ile Tyr Cys Arg Lys Lys Arg Ile Ser Ala Asn Pro  
 245 250 255  
 Thr Asn Pro Asp Glu Ala Asp Lys Val Gly Ala Glu Asn Thr Ile Thr  
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<211> 1303

<212> DNA

<213> homo sapiens

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<223> human FcRIIB1

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<212> DNA

<213> homo sapiens

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<223> human FcRIIB

<400> 29

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<211> 2372

<212> DNA

<213> homo sapiens

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<223> Human FcRIIa

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<211> 2009

<212> DNA

<213> homo sapiens

<220>

<223> Human IgG2

<400> 31

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<210> 32

<211> 326

<212> PRT

<213> homo sapiens

<220>

<223> Human IgG2

<400> 32

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Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	
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	50					55					60					
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	
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Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	
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Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
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		115					120					125				
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	130					135					140					
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
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				165					170					175		
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			180					185					190			
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	
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	210					215					220					
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	
225					230					235					240	
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	
				245					250					255		
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		260						265					270			
Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	
		275					280					285				
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	
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Ser Leu Ser Pro Gly Lys  
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<210> 33

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V1

<400> 33

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1224

<210> 34

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<223> sFCRIIIAG2-V1

<400> 34

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			20					25					30			
Ala	Tyr	Ser	Pro	Glu	Asp	Asn	Ser	Thr	Gln	Trp	Phe	His	Asn	Glu	Ser	
		35					40					45				
Leu	Ile	Ser	Ser	Gln	Ala	Ser	Ser	Tyr	Phe	Ile	Asp	Ala	Ala	Thr	Val	
	50					55					60					
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			100					105					110			
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	130					135					140					
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		195					200					205				
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	210					215					220					

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				245					250					255	
Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln
			260					265					270		
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		275					280					285			
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Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr
305					310					315					320
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
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Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
		355					360					365			
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
	370					375					380				
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
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<210> 35

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V2

<400> 35

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<210> 36

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V2

<400> 36

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 20          25          30

Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
 35          40          45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
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Pro	Arg	Trp	Val	Phe	Lys	Glu	Glu	Asp	Pro	Ile	His	Leu	Arg	Cys	His	
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Ser	Trp	Lys	Asn	Thr	Ala	Leu	His	Lys	Val	Thr	Tyr	Leu	Gln	Asn	Gly	
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Lys	Gly	Arg	Lys	Tyr	Phe	His	His	Asn	Ser	Asp	Phe	Tyr	Ile	Pro	Lys	
	130					135					140					
Ala	Thr	Leu	Lys	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Arg	Gly	Leu	Val	Gly	
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		195					200					205				
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	210					215					220					
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	
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			245						250					255		
Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	
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Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	
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Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	
305					310					315					320	
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	
			325						330					335		
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	
		340						345					350			
Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	
		355					360					365				
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	
	370					375					380					
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	



385

390

395

400

Ser Leu Ser Leu Ser Pro Gly Lys  
405

&lt;210&gt; 37

&lt;211&gt; 1230

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; sFcRIIIAG2-V3

&lt;400&gt; 37

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1230

<210> 38

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V3

<400> 38

Met	Arg	Thr	Glu	Asp	Leu	Pro	Lys	Ala	Val	Val	Phe	Leu	Glu	Pro	Gln
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Trp	Tyr	Arg	Val	Leu	Glu	Lys	Asp	Ser	Val	Thr	Leu	Lys	Cys	Gln	Gly
			20					25					30		

Ala	Tyr	Ser	Pro	Glu	Asp	Asn	Ser	Thr	Gln	Trp	Phe	His	Asn	Glu	Ser
		35					40					45			

Leu	Ile	Ser	Ser	Gln	Ala	Ser	Ser	Tyr	Phe	Ile	Asp	Ala	Ala	Thr	Val
50						55					60				

Asp	Asp	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Thr	Asn	Leu	Ser	Thr	Leu	Ser
65					70					75					80

Asp	Pro	Val	Gln	Leu	Glu	Val	His	Ile	Gly	Trp	Leu	Leu	Leu	Gln	Ala
			85						90					95	

Pro	Arg	Trp	Val	Phe	Lys	Glu	Glu	Asp	Pro	Ile	His	Leu	Arg	Cys	His
			100					105					110		

Ser	Trp	Lys	Asn	Thr	Ala	Leu	His	Lys	Val	Thr	Tyr	Leu	Gln	Asn	Gly
		115					120						125		

Lys	Gly	Arg	Lys	Tyr	Phe	His	His	Asn	Ser	Asp	Phe	Tyr	Ile	Pro	Lys
	130					135					140				

Ala	Thr	Leu	Lys	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Arg	Gly	Leu	Val	Gly
145					150					155					160

Ser	Lys	Asn	Val	Ser	Ser	Glu	Thr	Val	Asn	Ile	Thr	Val	Gln	Ala	Pro
			165						170					175	

Ser	Ser	Ser	Pro	Met	Glu	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro
			180					185					190		

Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
		195					200					205			

Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
	210					215						220			

Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp
225					230					235					240
Tyr	Val	Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
				245					250					255	
Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val
			260					265					270		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
		275					280					285			
Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly
	290					295					300				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu
305					310					315					320
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
				325					330					335	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
			340					345					350		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
		355					360					365			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
	370					375					380				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
385					390					395					400
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
				405					410						

<210> 39

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V4

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acacagtggg ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180  
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<210> 40

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<223> sFCRIIIAG2-V4

<400> 40

Met	Arg	Thr	Glu	Asp	Leu	Pro	Lys	Ala	Val	Val	Phe	Leu	Glu	Pro	Gln
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Trp	Tyr	Arg	Val	Leu	Glu	Lys	Asp	Ser	Val	Thr	Leu	Lys	Cys	Gln	Gly
			20					25					30		
Ala	Tyr	Ser	Pro	Glu	Asp	Asn	Ser	Thr	Gln	Trp	Phe	His	Asn	Glu	Ser
		35					40					45			

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val  
 50 55 60  
 Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser  
 65 70 75 80  
 Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala  
 85 90 95  
 Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His  
 100 105 110  
 Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly  
 115 120 125  
 Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys  
 130 135 140  
 Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly  
 145 150 155 160  
 Ser Lys Asn Val Ser Ser Glu Thr Val Thr Ile Thr Val Gln Ala Pro  
 165 170 175  
 Ser Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro  
 180 185 190  
 Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro  
 195 200 205  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 210 215 220  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp  
 225 230 235 240  
 Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 245 250 255  
 Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val  
 260 265 270  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 275 280 285  
 Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly  
 290 295 300  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
 305 310 315 320  
 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 325 330 335  
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 340 345 350  
 Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe  
 355 360 365  
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

370		375		380
Val Phe Ser Cys Ser	Val Met His Glu Ala Leu	His Asn His Tyr Thr		
385	390	395	400	

  

Gln Lys Ser Leu Ser	Leu Ser Pro Gly Lys
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<210> 41

<211> 1227

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIBG2-N297Q

<400> 41

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cagtggttcc acaatgggaa tctcattccc acccacacgc agcccagcta caggttcaag 180
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cctgtgcacg tgactgtgct ttctgagtgg ctgggtgctcc agacccctca cctggagttc 300
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atcccacaag caaaccacag tcacagtggg gattaccact gcacaggaaa cataggctac 480
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<210> 42

<211> 409

<212> PRT

<213> Homo sapiens

**<220>**

&lt;223&gt; sFcRIIBG2-N297Q

<400> 42

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20 25 30

His Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu  
35 40 45

Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn  
50 55 60

Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp  
65 70 75 80

Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro  
85 90 95

His Leu Glu Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser  
100 105 110

Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys  
115 120 125

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala  
130 135 140

Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr  
145 150 155 160

Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro Ser  
165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys  
180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
195 200 205

Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
210						215					220					
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	
225					230					235					240	
Val	Asp	Gly	Met	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
				245					250					255		
Gln	Phe	Gln	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	
			260					265					270			
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	
		275					280					285				
Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	
	290					295					300					
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	
305					310					315					320	
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
				325					330					335		
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
			340					345					350			
Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
		355					360					365				
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	
	370					375					380					
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
385					390					395					400	
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
				405												